

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Diane Pennica
- (ii) TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
- (iii) NUMBER OF SEQUENCES: 43
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/015089
 - (B) FILING DATE: 29-Jan-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hasak, Janet E.
 - (B) REGISTRATION NUMBER: 28,616
 - (C) REFERENCE/DOCKET NUMBER: P1056
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650/225-1896
 - (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2024 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GAACCCACCA GAAGGAAGAA ACTCCAAACA CATCCGAACA TCAGAAGGAG 50
CAAACCTCGTG ACACGCCACC TTTAAGAACC GTGACACTCA ACGCTAGGGT 100
CCGCGGCTTC ATTCTTGAAG TCAGTGAGAC CAAGAACCCA CCAATTCCGG 150
ACACGGCAAA GTAACATCCT AGACATGGCT TTAGAGATCC ACATGTCAGA 200
CCCCATGTGC CTCATCGAGA ACTTTAATGA GCAGCTGAAG GTTAATCAGG 250
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AAGCTTTGGA GATCCTGTCT GCCATTACGC AACCTGTAGT TGTGGTAGCG 300
ATTGTGGGCC TCTATCGCAC TGGCAAATCC TACCTGATGA ACAAGCTGGC 350
TGGGAAGAAC AAGGGCTTCT CTGTTGCATC TACGGTGCAG TCTCACACCA 400
AGGGAATTTG GATATGGTGT GTGCCTCATC CCAACTGGCC AAATCACACA 450
TTAGTTCTGC TTGACACCGA GGGCCTGGGA GATGTAGAGA AGGCTGACAA 500
CAAGAATGAT ATCCAGATCT TTGCACTGGC ACTCTTACTG AGCAGCACCT 550
TTGTGTACAA TACTGTGAAC AAAATTGATC AGGGTGCTAT CGACCTACTG 600
CACAATGTGA CAGAACTGAC AGATCTGCTC AAGGCAAGAA ACTCACCCGA 650
CCTTGACAGG GTTGAAGATC CTGCTGACTC TGCGAGCTTC TTCCCAGACT 700
TAGTGTGGAC TCTGAGAGAT TTCTGCTTAG GCCTGGAAAT AGATGGGCAA 750
CTTGTCACAC CAGATGAATA CCTGGAGAAT TCCCTAAGGC CAAAGCAAGG 800
TAGTGATCAA AGAGTTCAAA ATTTCAATTT GCCCCGTCTG TGTATACAGA 850
AGTTCTTTCC AAAAAAGAAA TGCTTTATCT TTGACTTACC TGCTCACCAA 900
AAAAAGCTTG CCCAACTTGA AACACTGCCT GATGATGAGC TAGAGCCTGA 950
ATTTGTGCAA CAAGTGACAG AATTCTGTTC CTACATCTTT AGCCATTCTA 1000
TGACCAAGAC TCTTCCAGGT GGCATCATGG TCAATGGATC TCGTCTAAAG 1050
AACCTGGTGC TGACCTATGT CAATGCCATC AGCAGTGGGG ATCTGCCTTG 1100
CATAGAGAAT GCAGTCCCTGG CCTTGGCTCA GAGAGAGAAC TCAGCTGCAG 1150
TGCAAAAGGC CATTGCCCAC TATGACCAGC AAATGGGCCA GAAAGTGCAG 1200
CTGCCCATGG AAACCCTCCA GGAGCTGCTG GACCTGCACA GGACCAGTGA 1250
GAGGGAGGCC ATTGAAGTCT TCATGAAAAA CTCTTTCAAG GATGTAGACC 1300
AAAGTTTCCA GAAAGAATTG GAGACTCTAC TAGATGCAAA ACAGAATGAC 1350
ATTTGTAAAC GGAACCTGGA AGCATCCTCG GATTATTGCT CGGCTTTACT 1400
TAAGGATATT TTTGGTCCTC TAGAAGAAGC AGTGAAGCAG GGAATTTATT 1450
CTAAGCCAGG AGGCCATAAT CTCTTCATTC AGAAAACAGA AGAACTGAAG 1500
GCAAAGTACT ATCGGGAGCC TCGGAAAGGA ATACAGGCTG AAGAAGTTCT 1550
GCAGAAATAT TTAAAGTCCA AGGAGTCTGT GAGTCATGCA ATATTACAGA 1600
CTGACCAGGC TCTCACAGAG ACGGAAAAAA AGAAGAAAGA GGCACAAGTG 1650
AAAGCAGAAG CTGAAAAGGC TGAAGCGCAA AGGTTGGCGG CGATTCAAAG 1700

GCAGAACGAG CAAATGATGC AGGAGAGGGA GAGACTCCAT CAGGAACAAG 1750
 TGAGACAAAT GGAGATAGCC AAACAAAATT GGCTGGCAGA GCAACAGAAA 1800
 ATGCAGGAAC AACAGATGCA GGTATTCATC AATTGTTTCA TCTCTCCCCT 1850
 GCCTGTAACG ATGAGAGTAT GTAGCAGTGG CAAAGAGGGA GAGGCAGCAA 1900
 GATCTTGTGG CTCTCAGCAG GGAGTCTGGA GCCAGAAAGT CTGGGTATGA 1950
 ATCCAAGCTC CACCTCTTAG TAAGTATATG GTTTAGGCAA GTTATCTATC 2000
 ACCTCTGTGC CTAATTTTCC TCCG 2024

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2024 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAGGAAAA TTAGGCACAG AGGTGATAGA TAACTTGCTT AAACCATATA 50
 CTTACTAAGA GGTGGAGCTT GGATTCATAC CCAGACTTTC TGGCTCCAGA 100
 CTCCCTGCTG AGAGCCACAA GATCTTGCTG CCTCTCCCTC TTTGCCACTG 150
 CTACATACTC TCATCGTTAC AGGCAGGGGA GAGATGAAAC AATTGATGAA 200
 TACCTGCATC TGTGTGTCCT GCATTTTCTG TTGCTCTGCC AGCCAATTTT 250
 GTTTGGCTAT CTCCATTTGT CTCACTTGTT CCTGATGGAG TCTCTCCCTC 300
 TCCTGCATCA TTTGCTCGTT CTGCCTTTGA ATCGCCGCCA ACCTTTGCGC 350
 TTCAGCCTTT TCAGCTTCTG CTTTCACTTG TGCCTCTTTC TTCTTTTTTT 400
 CCGTCTCTGT GAGAGCCTGG TCAGTCTGTA ATATTGCATG ACTCACAGAC 450
 TCCTTGGA CT TAAATATTT CTGCAGAACT TCTTCAGCCT GTATTCCTTT 500
 CCGAGGCTCC CGATAGTACT TTGCCTTCAG TTCTTCTGTT TTCTGAATGA 550
 AGAGATTATG GCCTCCTGGC TTAGAATAAA TTCCCTGCTT CACTGCTTCT 600
 TCTAGAGGAC CAAAAATATC CTTAAGTAAA GCCGAGCAAT AATCCGAGGA 650
 TGCTTCCAGG TTCCGTTTAC AAATGTCATT CTGTTTTGCA TCTAGTAGAG 700
 TCTCCAATTC TTTCTGGAAA CTTTGGTCTA CATCCTTGAA AGAGTTTTTC 750
 ATGAAGACTT CAATGGCCTC CCTCTCACTG GTCCTGTGCA GGTCCAGCAG 800
 CTCCTGGAGG GTTTCATG GCAGCTGCAC TTTCTGGCCC ATTTGCTGGT 850

CATAGTGGGC AATGGCCTTT TGCAGTGCAG CTGAGTTCTC TCTCTGAGCC 900
 AAGGCCAGGA CTGCATTCTC TATGCAAGGC AGATCCCCAC TGCTGATGGC 950
 ATTGACATAG GTCAGCACCA GGTTCCTTTAG ACGAGATCCA TTGACCATGA 1000
 TGCCACCTGG AAGAGTCTTG GTCATAGAAT GGCTAAAGAT GTAGGAACAG 1050
 AATTCTGTCA CTTGTTGCAC AAATTCAGGC TCTAGCTCAT CATCAGGCAG 1100
 TGTTTCAAGT TGGGCAAGCT TTTTTTGGTG AGCAGGTAAG TCAAAGATAA 1150
 AGCATTTCTT TTTTGGAAAG AACTTCTGTA TACACAGACG GGGCAAATTG 1200
 AAATTTTGAA CTCTTTGATC ACTACCTTGC TTTGGCCTTA GGGAATTCTC 1250
 CAGGTATTCA TCTGGTGTGA CAAGTTGCCC ATCTATTTCC AGGCCTAAGC 1300
 AGAAATCTCT CAGAGTCCAC ACTAAGTCTG GGAAGAAGCT CGCAGAGTCA 1350
 GCAGGATCTT CAACCCTGTC AAGGTCGGGT GAGTTTCTTG CCTTGAGCAG 1400
 ATCTGTCAGT TCTGTCACAT TGTGCAGTAG GTCGATAGCA CCCTGATCAA 1450
 TTTTGTTTAC AGTATTGTAC ACAAAGGTGC TGCTCAGTAA GAGTGCCAGT 1500
 GCAAAGATCT GGATATCATT CTTGTTGTCA GCCTTCTCTA CATCTCCCAG 1550
 GCCCTCGGTG TCAAGCAGAA CTAATGTGTG ATTTGGCCAG TTGGGATGAG 1600
 GCACACACCA TATCCAAATT CCCTTGGTGT GAGACTGCAC CGTAGATGCA 1650
 ACAGAGAAGC CCTTGTCTT CCCAGCCAGC TTGTTTATCA GGTAGGATTT 1700
 GCCAGTGCGA TAGAGGCCCA CAATCGCTAC CACAACCTACA GGTTGCGTAA 1750
 TGGCAGACAG GATCTCCAAA GCTTCCTGAT TAACCTTCAG CTGCTCATT 1800
 AAGTTCTCGA TGAGGCACAT GGGGTCTGAC ATGTGGATCT CTAAAGCCAT 1850
 GTCTAGGATG TTACTTTGCC GTGTCCGGAA TTGGTGGGTT CTTGGTCTCA 1900
 CTGACTTCAA GAATGAAGCC GCGGACCCTA GCGTTGAGTG TCACGGTTCT 1950
 TAAAGGTGGC GTGTCACGAG TTTGCTCCTT CTGATGTTTCG GATGTGTTTG 2000
 GAGTTTCTTC CTTCTGGTGG GTTC 2024

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Leu	Glu	Ile	His	Met	Ser	Asp	Pro	Met	Cys	Leu	Ile	Glu	1	5	10	15
Asn	Phe	Asn	Glu	Gln	Leu	Lys	Val	Asn	Gln	Glu	Ala	Leu	Glu	Ile	20	25	30	
Leu	Ser	Ala	Ile	Thr	Gln	Pro	Val	Val	Val	Val	Ala	Ile	Val	Gly	35	40	45	
Leu	Tyr	Arg	Thr	Gly	Lys	Ser	Tyr	Leu	Met	Asn	Lys	Leu	Ala	Gly	50	55	60	
Lys	Asn	Lys	Gly	Phe	Ser	Val	Ala	Ser	Thr	Val	Gln	Ser	His	Thr	65	70	75	
Lys	Gly	Ile	Trp	Ile	Trp	Cys	Val	Pro	His	Pro	Asn	Trp	Pro	Asn	80	85	90	
His	Thr	Leu	Val	Leu	Leu	Asp	Thr	Glu	Gly	Leu	Gly	Asp	Val	Glu	95	100	105	
Lys	Ala	Asp	Asn	Lys	Asn	Asp	Ile	Gln	Ile	Phe	Ala	Leu	Ala	Leu	110	115	120	
Leu	Leu	Ser	Ser	Thr	Phe	Val	Tyr	Asn	Thr	Val	Asn	Lys	Ile	Asp	125	130	135	
Gln	Gly	Ala	Ile	Asp	Leu	Leu	His	Asn	Val	Thr	Glu	Leu	Thr	Asp	140	145	150	
Leu	Leu	Lys	Ala	Arg	Asn	Ser	Pro	Asp	Leu	Asp	Arg	Val	Glu	Asp	155	160	165	
Pro	Ala	Asp	Ser	Ala	Ser	Phe	Phe	Pro	Asp	Leu	Val	Trp	Thr	Leu	170	175	180	
Arg	Asp	Phe	Cys	Leu	Gly	Leu	Glu	Ile	Asp	Gly	Gln	Leu	Val	Thr	185	190	195	
Pro	Asp	Glu	Tyr	Leu	Glu	Asn	Ser	Leu	Arg	Pro	Lys	Gln	Gly	Ser	200	205	210	
Asp	Gln	Arg	Val	Gln	Asn	Phe	Asn	Leu	Pro	Arg	Leu	Cys	Ile	Gln	215	220	225	
Lys	Phe	Phe	Pro	Lys	Lys	Lys	Cys	Phe	Ile	Phe	Asp	Leu	Pro	Ala	230	235	240	
His	Gln	Lys	Lys	Leu	Ala	Gln	Leu	Glu	Thr	Leu	Pro	Asp	Asp	Glu	245	250	255	
Leu	Glu	Pro	Glu	Phe	Val	Gln	Gln	Val	Thr	Glu	Phe	Cys	Ser	Tyr	260	265	270	
Ile	Phe	Ser	His	Ser	Met	Thr	Lys	Thr	Leu	Pro	Gly	Gly	Ile	Met	275	280	285	

Val	Asn	Gly	Ser	Arg	Leu	Lys	Asn	Leu	Val	Leu	Thr	Tyr	Val	Asn	
				290					295					300	
Ala	Ile	Ser	Ser	Gly	Asp	Leu	Pro	Cys	Ile	Glu	Asn	Ala	Val	Leu	
				305					310					315	
Ala	Leu	Ala	Gln	Arg	Glu	Asn	Ser	Ala	Ala	Val	Gln	Lys	Ala	Ile	
				320					325					330	
Ala	His	Tyr	Asp	Gln	Gln	Met	Gly	Gln	Lys	Val	Gln	Leu	Pro	Met	
				335					340					345	
Glu	Thr	Leu	Gln	Glu	Leu	Leu	Asp	Leu	His	Arg	Thr	Ser	Glu	Arg	
				350					355					360	
Glu	Ala	Ile	Glu	Val	Phe	Met	Lys	Asn	Ser	Phe	Lys	Asp	Val	Asp	
				365					370					375	
Gln	Ser	Phe	Gln	Lys	Glu	Leu	Glu	Thr	Leu	Leu	Asp	Ala	Lys	Gln	
				380					385					390	
Asn	Asp	Ile	Cys	Lys	Arg	Asn	Leu	Glu	Ala	Ser	Ser	Asp	Tyr	Cys	
				395					400					405	
Ser	Ala	Leu	Leu	Lys	Asp	Ile	Phe	Gly	Pro	Leu	Glu	Glu	Ala	Val	
				410					415					420	
Lys	Gln	Gly	Ile	Tyr	Ser	Lys	Pro	Gly	Gly	His	Asn	Leu	Phe	Ile	
				425					430					435	
Gln	Lys	Thr	Glu	Glu	Leu	Lys	Ala	Lys	Tyr	Tyr	Arg	Glu	Pro	Arg	
				440					445					450	
Lys	Gly	Ile	Gln	Ala	Glu	Glu	Val	Leu	Gln	Lys	Tyr	Leu	Lys	Ser	
				455					460					465	
Lys	Glu	Ser	Val	Ser	His	Ala	Ile	Leu	Gln	Thr	Asp	Gln	Ala	Leu	
				470					475					480	
Thr	Glu	Thr	Glu	Lys	Lys	Lys	Lys	Glu	Ala	Gln	Val	Lys	Ala	Glu	
				485					490					495	
Ala	Glu	Lys	Ala	Glu	Ala	Gln	Arg	Leu	Ala	Ala	Ile	Gln	Arg	Gln	
				500					505					510	
Asn	Glu	Gln	Met	Met	Gln	Glu	Arg	Glu	Arg	Leu	His	Gln	Glu	Gln	
				515					520					525	
Val	Arg	Gln	Met	Glu	Ile	Ala	Lys	Gln	Asn	Trp	Leu	Ala	Glu	Gln	
				530					535					540	
Gln	Lys	Met	Gln	Glu	Gln	Gln	Met	Gln	Val	Phe	Ile	Asn	Cys	Phe	
				545					550					555	
Ile	Ser	Pro	Leu	Pro	Val	Thr	Met	Arg	Val	Cys	Ser	Ser	Gly	Lys	
				560					565					570	

Glu Gly Glu Ala Ala Arg Ser Cys Gly Ser Gln Gln Gly Val Trp
575 580 585

Ser Gln Lys Val Trp Val
590 591

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 592 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Ser	Glu	Ile	His	Met	Thr	Gly	Pro	Met	Cys	Leu	Ile	Glu	1	5	10	15
Asn	Thr	Asn	Gly	Arg	Leu	Met	Ala	Asn	Pro	Glu	Ala	Leu	Lys	Ile	20	25	30	
Leu	Ser	Ala	Ile	Thr	Gln	Pro	Met	Val	Val	Val	Ala	Ile	Val	Gly	35	40	45	
Leu	Tyr	Arg	Thr	Gly	Lys	Ser	Tyr	Leu	Met	Asn	Lys	Leu	Ala	Gly	50	55	60	
Lys	Lys	Lys	Gly	Phe	Ser	Leu	Gly	Ser	Thr	Val	Gln	Ser	His	Thr	65	70	75	
Lys	Gly	Ile	Trp	Met	Trp	Cys	Val	Pro	His	Pro	Lys	Lys	Pro	Gly	80	85	90	
His	Ile	Leu	Val	Leu	Leu	Asp	Thr	Glu	Gly	Leu	Gly	Asp	Val	Glu	95	100	105	
Lys	Gly	Asp	Asn	Gln	Asn	Asp	Ser	Trp	Ile	Phe	Ala	Leu	Ala	Val	110	115	120	
Leu	Leu	Ser	Ser	Thr	Phe	Val	Tyr	Asn	Ser	Ile	Gly	Thr	Ile	Asn	125	130	135	
Gln	Gln	Ala	Met	Asp	Gln	Leu	Tyr	Tyr	Val	Thr	Glu	Leu	Thr	His	140	145	150	
Arg	Ile	Arg	Ser	Lys	Ser	Ser	Pro	Asp	Glu	Asn	Glu	Asn	Glu	Val	155	160	165	
Glu	Asp	Ser	Ala	Asp	Phe	Val	Ser	Phe	Phe	Pro	Asp	Phe	Val	Trp	170	175	180	
Thr	Leu	Arg	Asp	Phe	Ser	Leu	Asp	Leu	Glu	Ala	Asp	Gly	Gln	Pro	185	190	195	
Leu	Thr	Pro	Asp	Glu	Tyr	Leu	Thr	Tyr	Ser	Leu	Lys	Leu	Lys	Lys	200	205	210	

Gly	Thr	Ser	Gln	Lys	Asp	Glu	Thr	Phe	Asn	Leu	Pro	Arg	Leu	Cys	
				215					220					225	
Ile	Arg	Lys	Phe	Phe	Pro	Lys	Lys	Lys	Cys	Phe	Val	Phe	Asp	Arg	
				230					235					240	
Pro	Val	His	Arg	Arg	Lys	Leu	Ala	Gln	Leu	Glu	Lys	Leu	Gln	Asp	
				245					250					255	
Glu	Glu	Leu	Asp	Pro	Glu	Phe	Val	Gln	Gln	Val	Ala	Asp	Phe	Cys	
				260					265					270	
Ser	Tyr	Ile	Phe	Ser	Asn	Ser	Lys	Thr	Lys	Thr	Leu	Ser	Gly	Gly	
				275					280					285	
Ile	Gln	Val	Asn	Gly	Pro	Arg	Leu	Glu	Ser	Leu	Val	Leu	Thr	Tyr	
				290					295					300	
Val	Asn	Ala	Ile	Ser	Ser	Gly	Asp	Leu	Pro	Cys	Met	Glu	Asn	Ala	
				305					310					315	
Val	Leu	Ala	Leu	Ala	Gln	Ile	Glu	Asn	Ser	Ala	Ala	Val	Gln	Lys	
				320					325					330	
Ala	Ile	Ala	His	Tyr	Glu	Gln	Gln	Met	Gly	Gln	Lys	Val	Gln	Leu	
				335					340					345	
Pro	Thr	Glu	Ser	Leu	Gln	Glu	Leu	Leu	Asp	Leu	His	Arg	Asp	Ser	
				350					355					360	
Glu	Arg	Glu	Ala	Ile	Glu	Val	Phe	Ile	Arg	Ser	Ser	Phe	Lys	Asp	
				365					370					375	
Val	Asp	His	Leu	Phe	Gln	Lys	Glu	Leu	Ala	Ala	Gln	Leu	Glu	Lys	
				380					385					390	
Lys	Arg	Asp	Asp	Phe	Cys	Lys	Gln	Asn	Gln	Glu	Ala	Ser	Ser	Asp	
				395					400					405	
Arg	Cys	Ser	Gly	Leu	Leu	Gln	Val	Ile	Phe	Ser	Pro	Leu	Glu	Glu	
				410					415					420	
Glu	Val	Lys	Ala	Gly	Ile	Tyr	Ser	Lys	Pro	Gly	Gly	Tyr	Arg	Leu	
				425					430					435	
Phe	Val	Gln	Lys	Leu	Gln	Asp	Leu	Lys	Lys	Lys	Tyr	Tyr	Glu	Glu	
				440					445					450	
Pro	Arg	Lys	Gly	Ile	Gln	Ala	Glu	Glu	Ile	Leu	Gln	Thr	Tyr	Leu	
				455					460					465	
Lys	Ser	Lys	Glu	Ser	Met	Thr	Asp	Ala	Ile	Leu	Gln	Thr	Asp	Gln	
				470					475					480	
Thr	Leu	Thr	Glu	Lys	Glu	Lys	Glu	Ile	Glu	Val	Glu	Arg	Val	Lys	
				485					490					495	

Ala	Glu	Ser	Ala	Gln	Ala	Ser	Ala	Lys	Met	Leu	Gln	Glu	Met	Gln	
				500					505					510	
Arg	Lys	Asn	Glu	Gln	Met	Met	Glu	Gln	Lys	Glu	Arg	Ser	Tyr	Gln	
				515					520					525	
Glu	His	Leu	Lys	Gln	Leu	Thr	Glu	Lys	Met	Glu	Asn	Asp	Arg	Val	
				530					535					540	
Gln	Leu	Leu	Lys	Glu	Gln	Glu	Arg	Thr	Leu	Ala	Leu	Lys	Leu	Gln	
				545					550					555	
Glu	Gln	Glu	Gln	Leu	Leu	Lys	Glu	Gly	Phe	Gln	Lys	Glu	Ser	Arg	
				560					565					570	
Ile	Met	Lys	Asn	Glu	Ile	Gln	Asp	Leu	Gln	Thr	Lys	Met	Arg	Arg	
				575					580					585	
Arg	Lys	Ala	Cys	Thr	Ile	Ser									
				590		592									

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Pro	Glu	Ile	Asn	Leu	Pro	Gly	Pro	Met	Ser	Leu	Ile	Asp	
1				5					10					15	
Asn	Thr	Lys	Gly	Gln	Leu	Val	Val	Asn	Pro	Glu	Ala	Leu	Lys	Ile	
				20					25					30	
Leu	Ser	Ala	Ile	Thr	Gln	Pro	Val	Val	Val	Val	Ala	Ile	Val	Gly	
				35					40					45	
Leu	Tyr	Arg	Thr	Gly	Lys	Ser	Tyr	Leu	Met	Asn	Lys	Leu	Ala	Gly	
				50					55					60	
Lys	Lys	Asn	Gly	Phe	Ser	Leu	Gly	Ser	Thr	Val	Lys	Ser	His	Thr	
				65					70					75	
Lys	Gly	Ile	Trp	Met	Trp	Cys	Val	Pro	His	Pro	Lys	Lys	Pro	Glu	
				80					85					90	
His	Thr	Leu	Val	Leu	Leu	Asp	Thr	Glu	Gly	Leu	Gly	Asp	Ile	Glu	
				95					100					105	
Lys	Gly	Asp	Asn	Glu	Asn	Asp	Ser	Trp	Ile	Phe	Ala	Leu	Ala	Ile	
				110					115					120	
Leu	Leu	Ser	Ser	Thr	Phe	Val	Tyr	Asn	Ser	Met	Gly	Thr	Ile	Asn	
				125					130					135	

Gln	Gln	Ala	Met	Asp	Gln	Leu	His	Tyr	Val	Thr	Glu	Leu	Thr	Asp	
				140					145					150	
Arg	Ile	Lys	Ala	Asn	Ser	Ser	Pro	Gly	Asn	Asn	Ser	Val	Asp	Asp	
				155					160					165	
Ser	Ala	Asp	Phe	Val	Ser	Phe	Phe	Pro	Ala	Phe	Val	Trp	Thr	Leu	
				170					175					180	
Arg	Asp	Phe	Thr	Leu	Glu	Leu	Glu	Val	Asp	Gly	Glu	Pro	Ile	Thr	
				185					190					195	
Ala	Asp	Asp	Tyr	Leu	Glu	Leu	Ser	Leu	Lys	Leu	Arg	Lys	Gly	Thr	
				200					205					210	
Asp	Lys	Lys	Ser	Lys	Ser	Phe	Asn	Asp	Pro	Arg	Leu	Cys	Ile	Arg	
				215					220					225	
Lys	Phe	Phe	Pro	Lys	Arg	Lys	Cys	Phe	Val	Phe	Asp	Trp	Pro	Ala	
				230					235					240	
Pro	Lys	Lys	Tyr	Leu	Ala	His	Leu	Glu	Gln	Leu	Lys	Glu	Glu	Glu	
				245					250					255	
Leu	Asn	Pro	Asp	Phe	Ile	Glu	Gln	Val	Ala	Glu	Phe	Cys	Ser	Tyr	
				260					265					270	
Ile	Leu	Ser	His	Ser	Asn	Val	Lys	Thr	Leu	Ser	Gly	Gly	Ile	Ala	
				275					280					285	
Val	Asn	Gly	Pro	Arg	Leu	Glu	Ser	Leu	Val	Leu	Thr	Tyr	Val	Asn	
				290					295					300	
Ala	Ile	Ser	Ser	Gly	Asp	Leu	Pro	Cys	Met	Glu	Asn	Ala	Val	Leu	
				305					310					315	
Ala	Leu	Ala	Gln	Ile	Glu	Asn	Ser	Ala	Ala	Val	Glu	Lys	Ala	Ile	
				320					325					330	
Ala	His	Tyr	Glu	Gln	Gln	Met	Gly	Gln	Lys	Val	Gln	Leu	Pro	Thr	
				335					340					345	
Glu	Thr	Leu	Gln	Glu	Leu	Leu	Asp	Leu	His	Arg	Asp	Ser	Glu	Arg	
				350					355					360	
Glu	Ala	Ile	Glu	Val	Phe	Met	Lys	Asn	Ser	Phe	Lys	Asp	Val	Asp	
				365					370					375	
Gln	Met	Phe	Gln	Arg	Lys	Leu	Gly	Ala	Gln	Leu	Glu	Ala	Arg	Arg	
				380					385					390	
Asp	Asp	Phe	Cys	Lys	Gln	Asn	Ser	Lys	Ala	Ser	Ser	Asp	Cys	Cys	
				395					400					405	
Met	Ala	Leu	Leu	Gln	Asp	Ile	Phe	Gly	Pro	Leu	Glu	Glu	Asp	Val	
				410					415					420	

Lys	Gln	Gly	Thr	Phe	Ser	Lys	Pro	Gly	Gly	Tyr	Arg	Leu	Phe	Thr	425	430	435
Gln	Lys	Leu	Gln	Glu	Leu	Lys	Asn	Lys	Tyr	Tyr	Gln	Val	Pro	Arg	440	445	450
Lys	Gly	Ile	Gln	Ala	Lys	Glu	Val	Leu	Lys	Lys	Tyr	Leu	Glu	Ser	455	460	465
Lys	Glu	Asp	Val	Ala	Asp	Ala	Leu	Leu	Gln	Thr	Asp	Gln	Ser	Leu	470	475	480
Ser	Glu	Lys	Glu	Lys	Ala	Ile	Glu	Val	Glu	Arg	Ile	Lys	Ala	Glu	485	490	495
Ser	Ala	Glu	Ala	Ala	Lys	Lys	Met	Leu	Glu	Glu	Ile	Gln	Lys	Lys	500	505	510
Asn	Glu	Glu	Met	Met	Glu	Gln	Lys	Glu	Lys	Ser	Tyr	Gln	Glu	His	515	520	525
Val	Lys	Gln	Leu	Thr	Glu	Lys	Met	Glu	Arg	Asp	Arg	Ala	Gln	Leu	530	535	540
Met	Ala	Glu	Gln	Glu	Lys	Thr	Leu	Ala	Leu	Lys	Leu	Gln	Glu	Gln	545	550	555
Glu	Arg	Leu	Leu	Lys	Glu	Gly	Phe	Glu	Asn	Glu	Ser	Lys	Arg	Leu	560	565	570
Gln	Lys	Asp	Ile	Trp	Asp	Ile	Gln	Met	Arg	Ser	Lys	Ser	Leu	Glu	575	580	585
Pro	Ile	Cys	Asn	Ile	Leu										590	591	

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Cys	Val	Lys	Ala	Glu	Ser	Ala	Gln	Ala	Ser	Ala	Lys	Met	Val	1	5	10	15
Glu	Glu	Met	Gln	Ile	Lys	Tyr	Gln	Gln	Met	Met	Glu	Glu	Lys	Glu	20	25	30	
Lys	Ser	Tyr	Gln	Glu	His	Val	Lys	Gln	Leu	Thr	Glu	Lys	Met	Glu	35	40	45	
Asn	Asp	Arg	Val	Gln	Leu	Leu	Lys	Glu	Gln	Glu	Arg	Thr	Leu	Ala	50	55	60	

Leu Lys Leu Gln
64

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Xaa Xaa Xaa Xaa Gly Lys Ser
1 5 8

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Xaa Xaa Xaa Xaa Gly Lys Thr
1 5 8

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Xaa Xaa Gly
1 4

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn Lys Xaa Asp
1 4

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Lys Xaa Asp
1 4

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Xaa Xaa Xaa
1 4

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Glu	Ala	Pro	Ile	Cys	Leu	Val	Glu	Asn	Trp	Lys	Asn	Gln	Leu	
1				5					10					15	
Thr	Val	Asn	Leu	Glu	Ala	Ile	Arg	Ile	Leu	Glu	Gln	Ile	Ala	Gln	
			20						25					30	
Pro	Leu	Val	Val	Val	Ala	Ile	Val	Gly	Leu	Tyr	Arg	Thr	Gly	Lys	
			35						40					45	
Ser	Tyr	Leu	Met	Asn	Arg	Leu	Ala	Gly	Arg	Asn	His	Gly	Phe	Ser	
			50						55					60	
Leu	Gly	Ser	Thr	Val	Gln	Ser	Glu	Thr	Lys	Gly	Ile	Trp	Met	Trp	
			65						70					75	
Cys	Val	Pro	His	Pro	Thr	Lys	Pro	Thr	His	Thr	Leu	Val	Leu	Leu	
			80						85					90	
Asp	Thr	Glu	Gly	Leu	Gly	Asp	Val	Glu	Lys	Gly	Asp	Pro	Lys	Asn	
			95						100					105	
Asp	Ser	Trp	Ile	Phe	Ala	Leu	Ala	Val	Leu	Leu	Ser	Ser	Thr	Phe	
			110						115					120	
Val	Tyr	Asn	Ser	Met	Ser	Thr	Ile	Asn	Gln	Gln	Ala	Leu	Glu	Gln	
			125						130					135	
Leu	His	Phe	Val	Thr	Glu	Leu	Thr	Gln	Leu	Ile	Arg	Ala	Lys	Ser	
			140						145					150	
Ser	Pro	Arg	Glu	Asp	Lys	Val	Lys	Asp	Ser	Ser	Glu	Phe	Val	Gly	
			155						160					165	

Phe	Phe	Pro	Asp	Phe	Ile	Trp	Ala	Val	Arg	Asp	Phe	Ala	Leu	Glu	170	175	180
Leu	Lys	Leu	Asn	Gly	Arg	Pro	Ile	Thr	Glu	Asp	Glu	Tyr	Leu	Glu	185	190	195
Asn	Ala	Leu	Lys	Leu	Ile	Gln	Gly	Asp	Asn	Leu	Lys	Val	Gln	Gln	200	205	210
Ser	Asn	Met	Thr	Arg	Glu	Cys	Ile	Arg	Tyr	Phe	Phe	Pro	Val	Arg	215	220	225
Lys	Cys	Phe	Val	Phe	Asp	Arg	Pro	Thr	Ser	Asp	Lys	Arg	Leu	Leu	230	235	240
Leu	Gln	Ile	Glu	Asn	Val	Pro	Glu	Asn	Gln	Leu	Glu	Arg	Asn	Phe	245	250	255
Gln	Val	Glu	Ser	Glu	Lys	Phe	Cys	Ser	Tyr	Ile	Phe	Thr	Asn	Gly	260	265	270
Lys	Thr	Lys	Thr	Leu	Arg	Gly	Gly	Val	Ile	Val	Thr	Gly	Asn	Arg	275	280	285
Leu	Gly	Thr	Leu	Val	Gln	Thr	Tyr	Val	Asn	Ala	Ile	Asn	Ser	Gly	290	295	300
Thr	Val	Pro	Cys	Leu	Glu	Asn	Ala	Val	Thr	Thr	Leu	Ala	Gln	Arg	305	310	315
Glu	Asn	Ser	Ile	Ala	Val	Gln	Lys	Ala	Ala	Asp	His	Tyr	Ser	Glu	320	325	330
Gln	Met	Ala	Gln	Arg	Met	Arg	Leu	Pro	Thr	Asp	Thr	Leu	Gln	Glu	335	340	345
Leu	Leu	Thr	Val	His	Ala	Ala	Cys	Glu	Lys	Glu	Ala	Ile	Ala	Val	350	355	360
Phe	Met	Glu	His	Ser	Phe	Lys	Asp	Asp	Glu	Gln	Glu	Phe	Gln	Lys	365	370	375
Lys	Leu	Val	Val	Thr	Ile	Glu	Glu	Arg	Lys	Glu	Glu	Phe	Ile	Arg	380	385	390
Gln	Asn	Glu	Ala	Ala	Ser	Ile	Arg	His	Cys	Gln	Ala	Glu	Leu	Glu	395	400	405
Arg	Leu	Ser	Glu	Ser	Leu	Arg	Lys	Ser	Ile	Ser	Cys	Gly	Ala	Phe	410	415	420
Ser	Val	Pro	Gly	Gly	His	Ser	Leu	Tyr	Leu	Glu	Ala	Arg	Lys	Lys	425	430	435
Ile	Glu	Leu	Gly	Tyr	Gln	Gln	Val	Leu	Arg	Lys	Gly	Val	Lys	Ala	440	445	450

Lys	Glu	Val	Leu	Lys	Ser	Phe	Leu	Gln	Ser	Gln	Ala	Ile	Met	Glu	455	460	465
Asp	Ser	Ile	Leu	Gln	Ser	Asp	Lys	Ala	Leu	Thr	Asp	Gly	Glu	Arg	470	475	480
Ala	Ile	Ala	Ala	Glu	Arg	Thr	Lys	Lys	Glu	Val	Ala	Glu	Lys	Glu	485	490	495
Leu	Glu	Leu	Leu	Arg	Gln	Arg	Gln	Lys	Glu	Gln	Glu	Gln	Val	Met	500	505	510
Glu	Ala	Gln	Glu	Arg	Ser	Phe	Arg	Glu	Asn	Ile	Ala	Lys	Leu	Gln	515	520	525
Glu	Lys	Met	Glu	Ser	Glu	Lys	Glu	Met	Leu	Leu	Arg	Glu	Gln	Glu	530	535	540
Lys	Met	Leu	Glu	His	Lys	Leu	Lys	Val	Gln	Glu	Glu	Leu	Leu	Ile	545	550	555
Glu	Gly	Phe	Arg	Glu	Lys	Ser	Asp	Met	Leu	Lys	Asn	Glu	Ile	Ser	560	565	570
His	Leu	Arg	Glu	Glu	Met	Glu	Arg	Thr	Arg	Arg	Lys	Pro	Ser	Leu	575	580	585
Phe	Gly	Gln	Ile	Leu	Asp	Thr	Ile	Gly	Asn	Ala	Phe	Ile	Met	Ile	590	595	600
Leu	Pro	Gly	Ala	Gly	Lys	Leu	Phe	Gly	Val	Gly	Leu	Lys	Phe	Leu	605	610	615
Gly	Ser	Leu	Ser	Ser											620		

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 589 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Ser	Glu	Ile	His	Met	Ser	Glu	Pro	Met	Cys	Leu	Ile	Glu	1	5	10	15
Asn	Thr	Glu	Ala	Gln	Leu	Val	Ile	Asn	Gln	Glu	Ala	Leu	Arg	Ile	20	25	30	
Leu	Ser	Ala	Ile	Thr	Gln	Pro	Val	Val	Val	Val	Ala	Ile	Val	Gly	35	40	45	
Leu	Tyr	Arg	Thr	Gly	Lys	Ser	Tyr	Leu	Met	Asn	Lys	Leu	Ala	Gly	50	55	60	

Lys	Arg	Thr	Gly	Phe	Ser	Leu	Gly	Ser	Thr	Val	Gln	Ser	His	Thr	
				65					70					75	
Lys	Gly	Ile	Trp	Met	Trp	Cys	Val	Pro	His	Pro	Lys	Lys	Ala	Gly	
				80					85					90	
Gln	Thr	Leu	Val	Leu	Leu	Asp	Thr	Glu	Gly	Leu	Glu	Asp	Val	Glu	
				95					100					105	
Lys	Gly	Asp	Asn	Gln	Asn	Asp	Cys	Trp	Ile	Phe	Ala	Leu	Ala	Val	
				110					115					120	
Leu	Leu	Ser	Ser	Thr	Phe	Ile	Tyr	Asn	Ser	Ile	Gly	Thr	Ile	Asn	
				125					130					135	
Gln	Gln	Ala	Met	Asp	Gln	Leu	His	Tyr	Val	Thr	Glu	Leu	Thr	Asp	
				140					145					150	
Leu	Ile	Lys	Ser	Lys	Ser	Ser	Pro	Asp	Gln	Ser	Asp	Val	Asp	Asn	
				155					160					165	
Ser	Ala	Asn	Phe	Val	Gly	Phe	Phe	Pro	Ile	Phe	Val	Trp	Thr	Leu	
				170					175					180	
Arg	Asp	Phe	Ser	Leu	Asp	Leu	Glu	Phe	Asp	Gly	Glu	Ser	Ile	Thr	
				185					190					195	
Pro	Asp	Glu	Tyr	Leu	Glu	Thr	Ser	Leu	Ala	Leu	Arg	Lys	Gly	Thr	
				200					205					210	
Asp	Glu	Asn	Thr	Lys	Lys	Phe	Asn	Met	Pro	Arg	Leu	Cys	Ile	Arg	
				215					220					225	
Lys	Phe	Phe	Pro	Lys	Arg	Lys	Cys	Phe	Ile	Phe	Asp	Arg	Pro	Gly	
				230					235					240	
Asp	Arg	Lys	Gln	Leu	Ser	Lys	Leu	Glu	Trp	Ile	Gln	Glu	Asp	Gln	
				245					250					255	
Leu	Asn	Lys	Glu	Phe	Val	Glu	Gln	Val	Ala	Glu	Phe	Thr	Ser	Tyr	
				260					265					270	
Ile	Phe	Ser	Tyr	Ser	Gly	Val	Lys	Thr	Leu	Ser	Gly	Gly	Ile	Thr	
				275					280					285	
Val	Asn	Gly	Pro	Arg	Leu	Lys	Ser	Leu	Val	Gln	Thr	Tyr	Val	Ser	
				290					295					300	
Ala	Ile	Cys	Ser	Gly	Glu	Leu	Pro	Cys	Met	Glu	Asn	Ala	Val	Leu	
				305					310					315	
Thr	Leu	Ala	Gln	Ile	Glu	Asn	Ser	Ala	Ala	Val	Gln	Lys	Ala	Ile	
				320					325					330	
Thr	Tyr	Tyr	Glu	Glu	Gln	Met	Asn	Gln	Lys	Ile	His	Met	Pro	Thr	
				335					340					345	

Glu Thr Leu Gln	Glu Leu Leu Asp Leu	His Arg Thr Cys Glu Arg	350	355	360
Glu Ala Ile Glu	Val Phe Met Lys Asn Ser	Phe Lys Asp Val Asp	365	370	375
Gln Lys Phe Gln	Glu Glu Leu Gly Ala Gln	Leu Glu Ala Lys Arg	380	385	390
Asp Ala Phe Val	Lys Lys Asn Met Asp Met	Ser Ser Ala His Cys	395	400	405
Ser Asp Leu Leu	Glu Gly Leu Phe Ala His	Leu Glu Glu Glu Val	410	415	420
Lys Gln Gly Thr	Phe Tyr Lys Pro Gly Gly	Tyr Tyr Leu Phe Leu	425	430	435
Gln Arg Lys Gln	Glu Leu Glu Lys Lys Tyr	Ile Gln Thr Pro Gly	440	445	450
Lys Gly Leu Gln	Ala Glu Val Met Leu Arg	Lys Tyr Phe Glu Ser	455	460	465
Lys Glu Asp Leu	Ala Asp Thr Leu Leu Lys	Met Asp Gln Ser Leu	470	475	480
Thr Glu Lys Glu	Lys Gln Ile Glu Met Glu	Arg Ile Lys Ala Glu	485	490	495
Ala Ala Glu Ala	Ala Asn Arg Ala Leu Ala	Glu Met Gln Lys Lys	500	505	510
His Glu Met Leu	Met Glu Gln Lys Glu Gln	Ser Tyr Gln Glu His	515	520	525
Met Lys Gln Leu	Thr Glu Lys Met Glu Gln	Glu Arg Lys Glu Leu	530	535	540
Met Ala Glu Gln	Gln Arg Ile Ile Ser Leu	Lys Leu Gln Glu Gln	545	550	555
Glu Arg Leu Leu	Lys Gln Gly Phe Gln Asn	Glu Ser Leu Gln Leu	560	565	570
Arg Gln Glu Ile	Glu Lys Ile Lys Asn Met	Pro Pro Pro Arg Ser	575	580	585
Cys Thr Ile Leu			589		

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Asp	Met	Ala	Ser	Glu	Ile	His	Met	Leu	Gln	Pro	Met	Cys	Leu	1	5	10	15
Ile	Glu	Asn	Thr	Glu	Ala	His	Leu	Val	Ile	Asn	Gln	Glu	Ala	Leu	20	25	30	
Arg	Ile	Leu	Ser	Ala	Ile	Asn	Gln	Pro	Val	Val	Val	Val	Ala	Ile	35	40	45	
Val	Gly	Leu	Tyr	Arg	Thr	Gly	Lys	Ser	Tyr	Leu	Met	Asn	Lys	Leu	50	55	60	
Ala	Gly	Lys	Arg	Thr	Gly	Phe	Ser	Leu	Gly	Ser	Thr	Val	Gln	Ser	65	70	75	
His	Thr	Lys	Gly	Ile	Trp	Met	Trp	Cys	Val	Pro	His	Pro	Lys	Lys	80	85	90	
Ala	Gly	Gln	Thr	Leu	Val	Leu	Leu	Asp	Thr	Glu	Gly	Leu	Glu	Asp	95	100	105	
Val	Glu	Lys	Gly	Asp	Asn	Gln	Asn	Asp	Cys	Trp	Ile	Phe	Ala	Leu	110	115	120	
Ala	Val	Leu	Leu	Ser	Ser	Thr	Phe	Val	Tyr	Asn	Ser	Met	Gly	Thr	125	130	135	
Ile	Asn	Gln	Gln	Ala	Met	Asp	Gln	Leu	His	Tyr	Val	Thr	Glu	Leu	140	145	150	
Thr	Asp	Leu	Ile	Lys	Ser	Lys	Ser	Ser	Pro	Asp	Gln	Ser	Gly	Ile	155	160	165	
Asp	Asp	Ser	Ala	Asn	Phe	Val	Gly	Phe	Phe	Pro	Thr	Phe	Val	Trp	170	175	180	
Ala	Leu	Arg	Asp	Phe	Ser	Leu	Glu	Leu	Glu	Val	Asn	Gly	Lys	Leu	185	190	195	
Val	Thr	Pro	Asp	Glu	Tyr	Leu	Glu	His	Ser	Leu	Thr	Leu	Lys	Lys	200	205	210	
Gly	Ala	Asp	Lys	Lys	Thr	Lys	Ser	Phe	Asn	Glu	Pro	Arg	Leu	Cys	215	220	225	
Ile	Arg	Lys	Phe	Phe	Pro	Lys	Arg	Lys	Cys	Phe	Ile	Phe	Asp	Arg	230	235	240	
Pro	Ala	Leu	Arg	Lys	Gln	Leu	Cys	Lys	Leu	Glu	Thr	Leu	Gly	Glu	245	250	255	
Glu	Glu	Leu	Cys	Ser	Glu	Phe	Val	Glu	Gln	Val	Ala	Glu	Phe	Thr	260	265	270	
Ser	Tyr	Ile	Phe	Ser	Tyr	Ser	Ala	Val	Lys	Thr	Leu	Ser	Gly	Gly	275	280	285	

Ile	Ile	Val	Asn	Gly	Pro	Arg	Leu	Lys	Ser	Leu	Val	Gln	Thr	Tyr	290	295	300
Val	Gly	Ala	Ile	Ser	Ser	Gly	Ser	Leu	Pro	Cys	Met	Glu	Ser	Ala	305	310	315
Val	Leu	Thr	Leu	Ala	Gln	Ile	Glu	Asn	Ser	Ala	Ala	Val	Gln	Lys	320	325	330
Ala	Ile	Thr	His	Tyr	Glu	Glu	Gln	Met	Asn	Gln	Lys	Ile	Gln	Met	335	340	345
Pro	Thr	Glu	Thr	Leu	Gln	Glu	Leu	Leu	Asp	Leu	His	Arg	Leu	Ile	350	355	360
Glu	Arg	Glu	Ala	Ile	Glu	Ile	Phe	Leu	Lys	Asn	Ser	Phe	Lys	Asp	365	370	375
Val	Asp	Gln	Lys	Phe	Gln	Thr	Glu	Leu	Gly	Asn	Leu	Leu	Ile	Ser	380	385	390
Lys	Arg	Asp	Ala	Phe	Ile	Lys	Lys	Asn	Ser	Asp	Val	Ser	Ser	Ala	395	400	405
His	Cys	Ser	Asp	Leu	Ile	Glu	Asp	Ile	Phe	Gly	Pro	Leu	Glu	Glu	410	415	420
Glu	Val	Lys	Gln	Gly	Thr	Phe	Ser	Lys	Pro	Gly	Gly	Tyr	Phe	Leu	425	430	435
Phe	Leu	Gln	Met	Arg	Gln	Glu	Leu	Glu	Lys	Lys	Tyr	Asn	Gln	Ala	440	445	450
Pro	Gly	Lys	Gly	Leu	Glu	Ala	Glu	Ala	Val	Leu	Lys	Lys	Tyr	Phe	455	460	465
Glu	Ser	Lys	Glu	Asp	Ile	Val	Glu	Thr	Leu	Leu	Lys	Thr	Asp	Gln	470	475	480
Ser	Leu	Thr	Glu	Ala	Ala	Lys	Glu	Ile	Glu	Val	Glu	Arg	Ile	Lys	485	490	495
Ala	Glu	Thr	Ala	Glu	Ala	Ala	Asn	Arg	Glu	Leu	Ala	Glu	Lys	Gln	500	505	510
Glu	Lys	Phe	Glu	Leu	Met	Met	Gln	Gln	Lys	Glu	Glu	Ser	Tyr	Gln	515	520	525
Glu	His	Val	Arg	Gln	Leu	Thr	Glu	Lys	Met	Lys	Glu	Glu	Gln	Lys	530	535	540
Lys	Leu	Ile	Glu	Glu	Gln	Asp	Asn	Ile	Ile	Ala	Leu	Lys	Leu	Arg	545	550	555
Glu	Gln	Glu	Lys	Phe	Leu	Arg	Glu	Gly	Tyr	Glu	Asn	Glu	Ser	Lys	560	565	570

Lys Leu Leu Arg Glu Ile Glu Asn Met Lys Arg Arg Gln Ser Pro
575 580 585

Gly Lys Cys Thr Ile Leu
590 591

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn	Phe	His	Gly	Ile	Trp	Ser	Thr	Thr	Met	Asp	Pro	Ile	Xaa	Leu	1	5	10	15
Val	Lys	Asn	Gln	Asn	Asn	His	Leu	Thr	Val	Asn	Pro	Lys	Ala	Leu	20	25	30	
Lys	Ile	Leu	Gly	Glu	Ile	Cys	Gln	Pro	Val	Val	Val	Val	Thr	Ile	35	40	45	
Ala	Gly	Leu	Tyr	Arg	Thr	Gly	Lys	Ser	Tyr	Leu	Met	Asn	Arg	Leu	50	55	60	
Ala	Gly	Gln	Asn	His	Gly	Phe	Arg	Leu	Gly	Ser	Thr	Val	Arg	Ser	65	70	75	
Glu	Thr	Lys	Gly	Ile	Xaa	Met	Trp	Cys	Val	Pro	His	Pro	Xaa	Lys	80	85	90	
Xaa	Asp	His	Ile	Leu	Val	Leu	Leu	Gly	Thr	Pro	Arg	Gly			95	100	103	

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Ala	Ser	Lys	Val	His	Met	Pro	Glu	Pro	Gln	Cys	Leu	Ile	Glu	1	5	10	15
Asn	Ile	Asn	Gly	Arg	Leu	Ala	Val	Asn	Pro	Lys	Ala	Leu	Lys	Leu	20	25	30	
Leu	Ser	Ala	Ile	Lys	Gln	Pro	Leu	Val	Val	Val	Ala	Ile	Val	Gly	35	40	45	
Leu	Tyr	Arg	Thr	Gly	Lys	Ser	Tyr	Leu	Met	Asn	Lys	Leu	Ala	Xaa	50	55	60	

Lys Asn Lys Gly
64

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Asp	Thr	Pro	Val	Leu	Pro	Met	Pro	Ala	Pro	Leu	Arg	Leu	Val	1	5	10	15
Thr	Asn	Lys	Asp	Gly	Val	Leu	Ala	Leu	Asn	Thr	Ala	Ala	Leu	Ala	20	25	30	
Val	Leu	Arg	Ser	Val	Thr	Gln	Pro	Val	Val	Val	Ala	Ile	Ala	35	40	45		
Gly	Pro	Tyr	Arg	Thr	Gly	Lys	Ser	Phe	Leu	Met	Asn	Arg	Leu	Ala	50	55	60	
Gln	Lys	Arg	Thr	Gly	Phe	Pro	Leu	Gly	Pro	Thr	Val	Tyr	Ala	Glu	65	70	75	
Thr	Lys	Gly	Ile	Trp	Met	Trp	Cys	Leu	Pro	His	Pro	Arg	Gln	Pro	80	85	90	
Arg	Val	Thr	Leu	Val	Leu	Leu	Asp	Thr	Glu	Gly	Leu	Glu	Asp	Pro	95	100	105	
Asn	Lys	Asp	Asn	Asp	His	Ser	Asp	Ala	Trp	Ile	Phe	Thr	Leu	Ala	110	115	120	
Leu	Leu	Leu	Ser	Ser	Thr	Leu	Val	Tyr	Asn	Ser	Val	Gly	Thr	Ile	125	130	135	
Asp	Gln	Arg	Ala	Leu	Ser	Ser	Cys	Ala	Gly	Asn	Gly	Ala	Val	Arg	140	145	150	
Ala	His	Pro	Arg	Gly	Glu	Lys	Asp	Asn	Asn	Pro	Ala	Ser	Asn	Phe	155	160	165	
Val	Ser	Ile	Phe	Pro	Gly	Phe	Val	Trp	Thr	Val	Arg	Asp	Phe	Thr	170	175	180	
Leu	Gln	Leu	Arg	Asp	Gly	Glu	Lys	Thr	Leu	Ser	Glu	Asp	Glu	Tyr	185	190	195	
Leu	Glu	Asp	Val	Leu	Arg	Leu	Arg	Pro	Gly	Ala	Gly	Arg	Arg	Gln	200	205	210	
Glu	Arg	Asn	Glu	Leu	Arg	Arg	Cys	Leu	Pro	Asn	Phe	Phe	Pro	Arg	215	220	225	

Arg	Lys	Leu	Phe	Thr	Met	Glu	Arg	Pro	Ala	Ala	Asp	Ala	Asn	Leu	230	235	240
Thr	Arg	Leu	Glu	Glu	Leu	Arg	Glu	Asp	Glu	Leu	Gln	Pro	Gly	Phe	245	250	255
Arg	Lys	Gln	Val	Asp	Ala	Phe	Cys	Arg	Tyr	Ile	Trp	Glu	Glu	Ala	260	265	270
Pro	Val	Lys	Val	Leu	Pro	Gly	Gly	His	Gln	Val	Thr	Gly	Ser	Ala	275	280	285
Leu	Ala	Tyr	Leu	Val	Glu	Lys	Tyr	Met	Ala	Ala	Ile	Ser	Ser	Gly	290	295	300
Ser	Val	Pro	Cys	Val	Glu	Ser	Thr	Leu	Lys	Ala	Leu	Ala	Gln	Ala	305	310	315
Glu	Asn	Thr	Ala	Ala	Val	Gln	Val	Ala	Val	Ala	Glu	Tyr	Gln	Arg	320	325	330
Gly	Met	Glu	Gln	Gly	Leu	Val	Leu	Pro	Thr	Ala	Ser	Tyr	Asp	Ala	335	340	345
Leu	Leu	Ala	Val	His	Arg	Asp	Cys	Glu	Gln	Arg	Ala	Leu	Ala	Leu	350	355	360
Phe	Leu	Ser	Arg	Ala	Phe	Ala	Asp	His	Lys	His	Gln	Tyr	His	Asp	365	370	375
Glu	Leu	Val	His	Lys	Leu	Glu	Gly	Gln	Arg	Gly	Val	Leu	Pro	Ala	380	385	390
Gln	Gln	Gly	Gly	Val	Gly	Ala	Ala	Val	Pro	His	Gly	Ala	Ala	Gly	395	400	405
Ala	Val	Glu	Gly	Arg	Gly	Arg	Arg	Leu	Gln	Arg	Gly	Asp	Tyr	Val	410	415	420
Ala	Arg	Gly	Gly	Ala	Gln	Leu	Phe	Lys	Glu	Asp	Val	Asn	Arg	Val	425	430	435
Leu	Glu	Glu	Tyr	Lys	Gln	Arg	Pro	Asp	Lys	Gly	Val	Arg	Ala	Glu	440	445	450
Ala	Val	Leu	Lys	Glu	Phe	Leu	Arg	Glu	His	Glu	Gly	Leu	Ala	Gln	455	460	465
Val	Leu	Lys	Ala	Thr	Glu	Val	Gln	Leu	Glu	Leu	Ala	Glu	Arg	Gln	470	475	480
Gln	Glu	Ala	Ala	Ala	Ala	Glu	Ala	Glu	Ala	Ala	Arg	Lys	Ala	Thr	485	490	495
Glu	Ala	Trp	Arg	Glu	Asp	Gln	Lys	Arg	Ser	Met	Glu	Glu	His	Lys	500	505	510

Arg	Gln	Leu	Glu	Gln	Trp	Met	Lys	Lys	Glu	Lys	His	Thr	Trp	Glu	
				515					520					525	
Glu	Glu	Leu	Asn	Arg	Met	Leu	Glu	His	His	Arg	Lys	Glu	Tyr	Lys	
				530					535					540	
Ala	Leu	Leu	Gln	Glu	Gly	Phe	Arg	Arg	Glu	Ala	Ala	Ala	Lys	Glu	
				545					550					555	
Lys	Gln	Ile	Arg	Glu	Leu	Gln	Glu	Glu	Met	Arg	Ser	Cys	Asn	Cys	
				560					565					570	
Thr	Val	Leu													
				573											

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTTTGTACAA GCTT 14

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTAATACGAC TCACTATAGG GCTCGAGCGG CCGCCCGGGC AGGT 44

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Thr	Gly	Thr	Ala	Gly	Cys	Gly	Thr	Gly	Ala	Ala	Gly	Ala	Cys	Gly	
1				5				10					15		
Ala	Cys	Ala	Gly	Ala	Ala	Ala	Gly	Gly	Gly	Cys	Gly	Thr	Gly	Gly	
			20				25						30		
Thr	Gly	Cys	Gly	Gly	Ala	Gly	Gly	Gly	Cys	Gly	Gly	Thr			
			35				40					43			

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCTGCCCCG 10

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACCGCCCTCC G 11

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAATACGAC TCACTATAGG GC 22

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Thr Gly Thr Ala Gly Cys Gly Thr Gly Ala Ala Gly Ala Cys Gly
1 5 10 15

Ala Cys Ala Gly Ala Ala
20 21

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCGAGGGGCC GCCCGGGCAG GT 22

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGGCGTGGT GCGGAGGGCG GT 22

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACCACAGTCC ATGCCATCAC 20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TCCACCACCC TGTGCTGTA 20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTAATACGA CTCACTATAG GGCGAATTGG GCCCGACGTC GCATGCTCCC 50
GGCCGCCATG GCCGCGGGAT TATCACTAGT GCGGCCGCCT GCAGGTCGAC 100
CATATGGGAG AGCTCCCAAC GCGTTGGATG CATAGCTTGA GTATTCTATA 150
GTGTCACCTA AAT 163

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATTTAGGTGA CACTATAGAA TACTCAAGCT ATGCATCCAA CGCGTTGGGA 50
GCTCTCCCAT ATGGTCGACC TGCAGGCGGC CGCACTAGTG ATTATCCCGC 100
GGCCATGGCG GCCGGGAGCA TGCGACGTCG GGCCCAATTC GCCCTATAGT 150
GAGTCGTATT ACA 163

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1776 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGGCTTTAG AGATCCACAT GTCAGACCCC ATGTGCCTCA TCGAGAACTT 50
TAATGAGCAG CTGAAGGTTA ATCAGGAAGC TTTGGAGATC CTGTCTGCCA 100
TTACGCAACC TGTAGTTGTG GTAGCGATTG TGGGCCTCTA TCGCACTGGC 150
AAATCCTACC TGATGAACAA GCTGGCTGGG AAGAACAAGG GCTTCTCTGT 200
TGCATCTACG GTGCAGTCTC ACACCAAGGG AATTGGATA TGGTGTGTGC 250
CTCATCCCAA CTGGCCAAAT CACACATTAG TTCTGCTTGA CACCGAGGGC 300
CTGGGAGATG TAGAGAAGGC TGACAACAAG AATGATATCC AGATCTTTGC 350
ACTGGCACTC TTA CTGAGCA GCACCTTTGT GTACAATACT GTGAACAAAA 400
TTGATCAGGG TGCTATCGAC CTACTGCACA ATGTGACAGA ACTGACAGAT 450

CTGCTCAAGG CAAGAACTC ACCCGACCTT GACAGGGTTG AAGATCCTGC 500
 TGA CTCTGCG AGCTTCTTCC CAGACTTAGT GTGGACTCTG AGAGATTTCT 550
 GCTTAGGCCT GGAAATAGAT GGGCAACTTG TCACACCAGA TGAATACCTG 600
 GAGAATTCCC TAAGGCCAAA GCAAGGTAGT GATCAAAGAG TTCAAAATTT 650
 CAATTTGCCC CGTCTGTGTA TACAGAAGTT CTTTCCAAAA AAGAAATGCT 700
 TTATCTTTGA CTTACCTGCT CACCAAAAAA AGCTTGCCCA ACTTGAAACA 750
 CTGCCTGATG ATGAGCTAGA GCCTGAATTT GTGCAACAAG TGACAGAATT 800
 CTGTTCTTAC ATCTTTAGCC ATTCTATGAC CAAGACTCTT CCAGGTGGCA 850
 TCATGGTCAA TGGATCTCGT CTAAAGAACC TGGTGCTGAC CTATGTCAAT 900
 GCCATCAGCA GTGGGGATCT GCCTTGCATA GAGAATGCAG TCCTGGCCTT 950
 GGCTCAGAGA GAGAACTCAG CTGCAGTGCA AAAGGCCATT GCCCACTATG 1000
 ACCAGCAAAT GGGCCAGAAA GTGCAGCTGC CCATGGAAAC CCTCCAGGAG 1050
 CTGCTGGACC TGCACAGGAC CAGTGAGAGG GAGGCCATTG AAGTCTTCAT 1100
 GAAAACTCT TTCAAGGATG TAGACCAAAG TTTCCAGAAA GAATTGGAGA 1150
 CTCTACTAGA TGCAAAACAG AATGACATTT GTAAACGGAA CCTGGAAGCA 1200
 TCCTCGGATT ATTGCTCGGC TTTACTTAAG GATATTTTTG GTCCTCTAGA 1250
 AGAAGCAGTG AAGCAGGGAA TTTATTCTAA GCCAGGAGGC CATAATCTCT 1300
 TCATTCAGAA AACAGAAGAA CTGAAGGCAA AGTACTATCG GGAGCCTCGG 1350
 AAAGGAATAC AGGCTGAAGA AGTTCTGCAG AAATATTTAA AGTCCAAGGA 1400
 GTCTGTGAGT CATGCAATAT TACAGACTGA CCAGGCTCTC ACAGAGACGG 1450
 AAAAAAGAA GAAAGAGGCA CAAGTGAAAG CAGAAGCTGA AAAGGCTGAA 1500
 GCGCAAAGGT TGGCGGCGAT TCAAAGGCAG AACGAGCAAA TGATGCAGGA 1550
 GAGGGAGAGA CTCCATCAGG AACAAGTGAG ACAAATGGAG ATAGCCAAAC 1600
 AAAATTGGCT GGCAGAGCAA CAGAAAATGC AGGAACAACA GATGCAGGTA 1650
 TTCATCAATT GTTTCATCTC TCCCCTGCCT GTAACGATGA GAGTATGTAG 1700
 CAGTGGCAAA GAGGGAGAGG CAGCAAGATC TTGTGGCTCT CAGCAGGGAG 1750
 TCTGGAGCCA GAAAGTCTGG GTATGA 1776

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Gly Ser His His His His
1 5 7

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Thr Gly Gly Cys Cys Cys Ala Thr Gly Cys Thr Cys Thr Gly
1 5 10 15

Gly Cys Ala Gly Ala Gly Gly Gly
20 23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Cys Ala Cys Cys Ala Cys Cys Cys Ala Cys Ala Ala Gly Gly
1 5 10 15

Ala Ala Gly Cys Cys Ala Thr Cys Cys
20 24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Cys Cys Gly Gly Ala Cys Ala Cys Gly Gly Cys Ala Ala Ala Gly
1 5 10 15

Thr Ala Ala Cys Ala Thr Cys Cys Thr
20 24

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gly Thr Ala Cys Ala Ala Thr Ala Cys Thr Gly Thr Gly Ala Ala
1 5 10 15
Cys Ala Ala Ala Ala Thr Thr Gly
20 23

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Thr Gly Cys Thr Ala Thr Cys Gly Ala Cys Cys Thr
1 5 10 15
Ala Cys Thr Gly Cys Ala Cys
20 22

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Ala Gly Thr Cys Ala Gly Cys Ala Gly Gly Ala Thr Cys Thr
1 5 10 15
Thr Cys Ala Ala Cys Cys Cys Thr Gly
20 24

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Thr Gly Cys Ala Gly Cys Thr Gly Cys Cys Cys Ala Thr Gly
1 5 10 15

Gly Ala Ala Ala Cys Cys Cys Thr Cys
20 24

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Cys Thr Gly Cys Thr Gly Ala Gly Ala Gly Cys Cys Ala Cys Ala
1 5 10 15

Ala Gly Ala Thr Cys Thr Thr Gly Cys
20 24

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Cys Cys Cys Ala Gly Ala Cys Thr Thr Thr Cys Thr Gly Gly Cys
1 5 10 15

Thr Cys Cys Ala Gly Ala Cys Thr Cys
20 24

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Arg Glu Ser His His His His His His Gly Ser
1 5 10 12